

SEQUENCE LISTING



<110> Durrant, Linda G  
Spendlove, Ian  
Hewett, Peter W  
Ramage, Judith M

<120> Anti-angiogenic vaccines: substances and methods  
relating thereto

<130> 0380-P02286US0

<140> US 09/623,063

<141> 2000-10-24

<150> PCT/GB99/00583

<151> 1999-02-26

<150> GB 9804121.3

<151> 1998-02-26

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1124

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source  
uncertain

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Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu  
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Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly  
35 40 45

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu  
50 55 60

Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg  
65 70 75 80

Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile  
85 90 95

Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg  
100 105 110

Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr  
115 120 125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys  
130 135 140

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Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser  
 145 150 155 160  
 Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val  
 165 170 175  
 His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg  
 180 185 190  
 Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val  
 195 200 205  
 Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys  
 210 215 220  
 Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys  
 225 230 235 240  
 Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu  
 245 250 255  
 Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu  
 260 265 270  
 Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser  
 275 280 285  
 Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro  
 290 295 300  
 Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly  
 305 310 315 320  
 Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln  
 325 330 335  
 Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile  
 340 345 350  
 Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro  
 355 360 365  
 Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr  
 370 375 380  
 Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His  
 385 390 395 400  
 Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro  
 405 410 415  
 Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met  
 420 425 430  
 Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu  
 435 440 445  
 Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn  
 450 455 460  
 Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys  
 465 470 475 480

Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln  
 485 490 495  
 Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu  
 500 505 510  
 Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly  
 515 520 525  
 His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro  
 530 535 540  
 Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn  
 545 550 555 560  
 Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val  
 565 570 575  
 Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys  
 580 585 590  
 Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg  
 595 600 605  
 Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu  
 610 615 620  
 Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro  
 625 630 635 640  
 Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val  
 645 650 655  
 Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile  
 660 665 670  
 Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys  
 675 680 685  
 Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro  
 690 695 700  
 Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser  
 705 710 715 720  
 Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln  
 725 730 735  
 Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu  
 740 745 750  
 Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile  
 755 760 765  
 Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala  
 770 775 780  
 Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr  
 785 790 795 800  
 Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr  
 805 810 815

Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu  
 820 825 830

Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu  
 835 840 845

Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp  
 850 855 860

Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly  
 865 870 875 880

His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly  
 885 890 895

Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp  
 900 905 910

Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile  
 915 920 925

Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe  
 930 935 940

Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe  
 945 950 955 960

Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr  
 965 970 975

Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr  
 980 985 990

Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu  
 995 1000 1005

Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr  
 1010 1015 1020

Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys  
 1025 1030 1035 1040

Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg  
 1045 1050 1055

Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg  
 1060 1065 1070

Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile  
 1075 1080 1085

Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn  
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Glu Glu Ala Ala

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 <212> PRT  
 <213> Unknown Organism

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           20                    25                    30  
 Leu Thr Asp Pro Gln Arg Phe Phe Leu Thr Cys Val Ser Gly Glu Ala  
           35                    40                    45  
 Gly Ala Gly Arg Gly Ser Asp Ala Trp Gly Pro Pro Leu Leu Leu Glu  
       50                    55                    60  
 Lys Asp Asp Arg Ile Val Arg Thr Pro Pro Gly Pro Pro Leu Arg Leu  
       65                    70                    75                    80  
 Ala Arg Asn Gly Ser His Gln Val Thr Leu Arg Gly Phe Ser Lys Pro  
           85                    90                    95  
 Ser Asp Leu Val Gly Val Phe Ser Cys Val Gly Gly Ala Gly Ala Arg  
           100                    105                    110  
 Arg Thr Arg Val Ile Tyr Val His Asn Ser Pro Gly Ala His Leu Leu  
           115                    120                    125  
 Pro Asp Lys Val Thr His Thr Val Asn Lys Gly Asp Thr Ala Val Leu  
       130                    135                    140  
 Ser Ala Arg Val His Lys Glu Lys Gln Thr Asp Val Ile Trp Lys Ser  
       145                    150                    155                    160  
 Asn Gly Ser Tyr Phe Tyr Thr Leu Asp Trp His Glu Ala Gln Asp Gly  
           165                    170                    175  
 Arg Phe Leu Leu Gln Leu Pro Asn Val Gln Pro Pro Ser Ser Gly Ile  
           180                    185                    190  
 Tyr Ser Ala Thr Tyr Leu Glu Ala Ser Pro Leu Gly Ser Ala Phe Phe  
           195                    200                    205  
 Arg Leu Ile Val Arg Gly Cys Gly Ala Gly Arg Trp Gly Pro Gly Cys  
       210                    215                    220  
 Thr Lys Glu Cys Pro Gly Cys Leu His Gly Gly Val Cys His Asp His  
       225                    230                    235                    240  
 Asp Gly Glu Cys Val Cys Pro Pro Gly Phe Thr Gly Thr Arg Cys Glu  
           245                    250                    255  
 Gln Ala Cys Arg Glu Gly Arg Phe Gly Gln Ser Cys Gln Glu Gln Cys  
           260                    265                    270  
 Pro Gly Ile Ser Gly Cys Arg Gly Leu Thr Phe Cys Leu Pro Asp Pro  
       275                    280                    285

Tyr Gly Cys Ser Cys Gly Ser Gly Trp Arg Gly Ser Gln Cys Gln Glu  
 290 295 300  
 Ala Cys Ala Pro Gly His Phe Gly Ala Asp Cys Arg Leu Gln Cys Gln  
 305 310 315 320  
 Cys Gln Asn Gly Gly Thr Cys Asp Arg Phe Ser Gly Cys Val Cys Pro  
 325 330 335  
 Ser Gly Trp His Gly Val His Cys Glu Lys Ser Asp Arg Ile Pro Gln  
 340 345 350  
 Ile Leu Asn Met Ala Ser Glu Leu Glu Phe Asn Leu Glu Thr Met Pro  
 355 360 365  
 Arg Ile Asn Cys Ala Ala Ala Gly Asn Pro Phe Pro Val Arg Gly Ser  
 370 375 380  
 Ile Glu Leu Arg Lys Pro Asp Gly Thr Val Leu Leu Ser Thr Lys Ala  
 385 390 395 400  
 Ile Val Glu Pro Glu Lys Thr Thr Ala Glu Phe Glu Val Pro Arg Leu  
 405 410 415  
 Val Leu Ala Asp Ser Gly Phe Trp Glu Cys Arg Val Ser Thr Ser Gly  
 420 425 430  
 Gly Gln Asp Ser Arg Arg Phe Lys Val Asn Val Lys Val Pro Pro Val  
 435 440 445  
 Pro Leu Ala Ala Pro Arg Leu Leu Thr Lys Gln Ser Arg Gln Leu Val  
 450 455 460  
 Val Ser Pro Leu Val Ser Phe Ser Gly Asp Gly Pro Ile Ser Thr Val  
 465 470 475 480  
 Arg Leu His Tyr Arg Pro Gln Asp Ser Thr Met Asp Trp Ser Thr Ile  
 485 490 495  
 Val Val Asp Pro Ser Glu Asn Val Thr Leu Met Asn Leu Arg Pro Lys  
 500 505 510  
 Thr Gly Tyr Ser Val Arg Val Gln Leu Ser Arg Pro Gly Glu Gly Gly  
 515 520 525  
 Glu Gly Ala Trp Gly Pro Pro Thr Leu Met Thr Thr Asp Cys Pro Glu  
 530 535 540  
 Pro Leu Leu Gln Pro Trp Leu Glu Gly Trp His Val Glu Gly Thr Asp  
 545 550 555 560  
 Arg Leu Arg Val Ser Trp Ser Leu Pro Leu Val Pro Gly Pro Leu Val  
 565 570 575  
 Gly Asp Gly Phe Leu Leu Arg Leu Trp Asp Gly Thr Arg Gly Gln Glu  
 580 585 590  
 Arg Arg Glu Asn Val Ser Ser Pro Gln Ala Arg Thr Ala Leu Leu Thr  
 595 600 605  
 Gly Leu Thr Pro Gly Thr His Tyr Gln Leu Asp Val Gln Leu Tyr His  
 610 615 620

Cys Thr Leu Leu Gly Pro Ala Ser Pro Pro Ala His Val Leu Leu Pro  
 625 630 635 640  
 Pro Ser Gly Pro Pro Ala Pro Arg His Leu His Ala Gln Ala Leu Ser  
 645 650 655  
 Asp Ser Glu Ile Gln Leu Thr Trp Lys His Pro Glu Ala Leu Pro Gly  
 660 665 670  
 Pro Ile Ser Lys Tyr Val Val Glu Val Gln Val Ala Gly Gly Ala Gly  
 675 680 685  
 Asp Pro Leu Trp Ile Asp Val Asp Arg Pro Glu Glu Thr Ser Thr Ile  
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 Ile Arg Gly Leu Asn Ala Ser Thr Arg Tyr Leu Phe Arg Met Arg Ala  
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 Ser Ile Gln Gly Leu Gly Asp Trp Ser Asn Thr Val Glu Glu Ser Thr  
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 Ala Glu Glu Gly Leu Asp Gln Gln Leu Ile Leu Ala Val Val Gly Ser  
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 Val Ser Ala Thr Cys Leu Thr Ile Leu Ala Ala Leu Leu Thr Leu Val  
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 Cys Ile Arg Arg Ser Cys Leu His Arg Arg Arg Thr Phe Thr Tyr Gln  
 785 790 795 800  
 Ser Gly Ser Gly Glu Glu Thr Ile Leu Gln Phe Ser Ser Gly Thr Leu  
 805 810 815  
 Thr Leu Thr Arg Arg Pro Lys Leu Gln Pro Glu Pro Leu Ser Tyr Pro  
 820 825 830  
 Val Leu Glu Trp Glu Asp Ile Thr Phe Glu Asp Leu Ile Gly Glu Gly  
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 Asn Phe Gly Gln Val Ile Arg Ala Met Ile Lys Lys Asp Gly Leu Lys  
 850 855 860  
 Met Asn Ala Ala Ile Lys Met Leu Lys Glu Tyr Ala Ser Glu Asn Asp  
 865 870 875 880  
 His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly His  
 885 890 895  
 His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Lys Asn Arg Gly Tyr  
 900 905 910  
 Leu Tyr Ile Ala Ile Glu Tyr Ala Pro Tyr Gly Asn Leu Leu Asp Phe  
 915 920 925  
 Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Arg Glu  
 930 935 940  
 His Gly Thr Ala Ser Thr Leu Ser Ser Arg Gln Leu Leu Arg Phe Ala  
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<210> 5  
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 <212> PRT  
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 <220>  
 <223> Description of Unknown Organism: Sequence source  
           uncertain  
  
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 <211> 9  
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 <211> 9  
 <212> PRT  
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 <220>  
 <223> Description of Unknown Organism: Sequence source  
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 Asn Gln His Gln Asp Pro Leu Glu Val  
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 <211> 9  
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 <220>  
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 Pro Arg His Glu Val Pro Asp Ile Leu  
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 <210> 9  
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uncertain

<400> 9

Lys Ile Val Asp Leu Pro Asp His Ile  
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<210> 10

<211> 10

<212> PRT

<213> Unknown Organism

<220>

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uncertain

<400> 10

Gly Ile Pro Arg Met Thr Pro Lys Ile Val  
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<210> 11

<211> 9

<212> PRT

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<220>

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<400> 11

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<210> 12

<211> 9

<212> PRT

<213> Unknown Organism

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uncertain

<400> 12

Ile Leu Ile Asn Ser Leu Pro Leu Val  
1 5

<210> 13

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source  
uncertain

<400> 13

Ile Val Asp Leu Pro Asp His Ile Glu Val  
1 5 10

<210> 14  
<211> 20  
<212> PRT  
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<220>  
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uncertain

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Pro Leu Glu Val  
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<211> 57  
<212> PRT  
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uncertain

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Ile Gly Arg Asp Phe Glu Ala Leu Met Asn Gln His Gln Asp Pro Leu  
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Glu Val Thr Gln Asp Val Thr Arg Glu Trp Ala Lys Lys Val Val Trp  
35 40 45  
Lys Arg Glu Lys Ala Ser Lys Ile Asn  
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<212> PRT  
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<220>  
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uncertain

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<210> 17  
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